



STIC Search Report

Biotech-Chem Library

File Copy
10/006591
updated

STIC Database Tracking Number: 10/006591

TO: David Lamberston
Location: REM-2B79/2C70
Art Unit: 1636
Friday, June 03, 2005

Case Serial Number: 10/006591

From: Toby Port
Location: Biotech-Chem Library
REM1-A59
Phone: 272-2523
toby.port@uspto.gov

Search Notes

Dear Examiner Lamberston,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: June 1, 2005, 18:46:12 ; Search time 71.2689 Seconds
(without alignments)

Title: US-10-006-591A-8

Perfect score: 33

Sequence: 1 ttgttccaaaggatttggctcttttttgttc 33

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:
1: /cggn2_6/patdata/1/ina/5A_COMB_seq:
2: /cggn2_6/patdata/1/ina/5B_COMB_seq:
3: /cggn2_6/patdata/1/ina/6A_COMB_seq:
4: /cggn2_6/patdata/1/ina/6B_COMB_seq:
5: /cggn2_6/patdata/1/ina/PCUTS_COMB_seq:
6: /cggn2_6/patdata/1/ina/backfile1.seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
C 1	33	100.0	687	1	US-08-300-386A-1	Sequence 1, Appli
C 2	33	100.0	687	3	US-08-331-645-1	Sequence 1, Appli
C 3	33	100.0	687	5	PCT-US94-01258-1	Sequence 1, Appli
C 4	33	100.0	687	5	PCT-US95-11235-1	Sequence 1, Appli
C 5	33	100.0	699	2	US-08-480-753-1	Sequence 1, Appli
C 6	33	100.0	699	3	US-09-041-089-8	Sequence 8, Appli
C 7	33	100.0	699	3	US-08-031-058-8	Sequence 8, Appli
C 8	33	100.0	699	4	US-09-011-064-6	Sequence 8, Appli
C 9	33	100.0	732	2	US-08-480-553-3	Sequence 3, Appli
C 10	33	100.0	1418	3	US-08-793-450-7	Sequence 7, Appli
C 11	33	100.0	1428	1	US-08-088-376-17	Sequence 17, Appli
C 12	33	100.0	1428	1	US-08-488-376-19	Sequence 19, Appli
C 13	33	100.0	1428	2	US-08-634-223-17	Sequence 17, Appli
C 14	33	100.0	1428	2	US-08-634-223-19	Sequence 19, Appli
C 15	33	100.0	1428	2	US-08-634-224-17	Sequence 17, Appli
C 16	33	100.0	1428	2	US-08-634-224-19	Sequence 19, Appli
C 17	33	100.0	1428	2	US-08-634-400-17	Sequence 17, Appli
C 18	33	100.0	1428	2	US-08-634-400-19	Sequence 19, Appli
C 19	33	100.0	1428	2	US-08-634-678-17	Sequence 17, Appli
C 20	33	100.0	1428	2	US-08-635-078-19	Sequence 19, Appli
C 21	33	100.0	1428	2	US-08-770-057-17	Sequence 17, Appli
C 22	33	100.0	1428	2	US-08-770-057-17	Sequence 17, Appli
C 23	33	100.0	1428	3	US-09-335-697B-17	Sequence 17, Appli
C 24	33	100.0	1428	3	US-09-335-697B-19	Sequence 19, Appli
C 25	33	100.0	1428	3	US-09-335-697B-17	Sequence 17, Appli
C 26	33	100.0	1428	3	US-09-335-697B-19	Sequence 19, Appli
C 27	33	100.0	1428	4	US-09-740-002-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-300-386A-1/C
; Sequence 1, Application.US/08300386A
; Patent No. 5667988

; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Dennis R
; APPLICANT: Kerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5667988th Torrey Pines Road, TPCB
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,674
; FILING DATE: 28-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,566
; FILING DATE: 02-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas B
; REGISTRATION NUMBER: 34,163
; FILING DATE: 02-SEP-1994
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 base pairs
; TYPE: nucleic acid

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005; 13:55:57 ; Search time 243.756 Seconds

(without alignments)

801.421 Million cell updates/sec

Title: US-10-006-591A-8
Perfect score: 33

Sequence: 1 ttgtcacaaatttggctctgttttttgtc 33

Scoring table: IDENTITY_NUC
GapOp 10.0 , Gapext 1.0

Searched: 4390206 seqB, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_GenesEq_16Dec04:
1: GenesEqn1980b;*
2: GenesEqn1980b;*
3: GenesEqn2000b;*
4: GenesEqn2001as;*
5: GenesEqn2001bs;*
6: GenesEqn2002as;*
7: GenesEqn2002bs;*
8: GenesEqn2003as;*
9: GenesEqn2003bs;*
10: GenesEqn2003cb;*
11: GenesEqn2003ds;*
12: GenesEqn2004as;*
13: GenesEqn2004bb;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description	
1	33	100.0	33	6 ABN84084	Abn84084 Heavy cha	
c 2	33	100.0	59	6 ABN84085	Abn84085 Antibody	
c 3	33	100.0	681	13 ADQ98070	Adq98070 Chimeric	
c 4	33	100.0	681	13 ADQ98075	Adq98075 Chimeric	
c 5	33	100.0	681	13 ADQ98086	Adq98086 Chimeric	
c 6	7	33	100.0	681	13 ADQ98087	Adq98087 Chimeric
c 7	7	33	100.0	681	13 ADQ98088	Adq98088 Chimeric
c 8	33	100.0	681	13 ADQ98089	Adq98089 Chimeric	
c 9	33	100.0	687	2 AAT15202	Aat15202 pC3Ap313	
c 10	33	100.0	699	2 AAT86666	Aat86666 DNA encod	
c 11	33	100.0	699	2 AAT44088	Aat44088 Ulcerativ	
c 12	33	100.0	699	2 ADB5154	Adb5154 p-ANCA re	
c 13	33	100.0	699	2 AAV51394	AAv51394 UC pANCA	
c 14	33	100.0	699	2 AAX91122	Aax91122 NANUC-2 a	
c 15	33	100.0	699	2 AAZ90667	AAz90667 UC pANCA	
c 16	33	100.0	732	2 AAT44089	Aat44089 Ulcerativ	
c 17	33	100.0	732	2 ADB51516	Adb51516 p-ANCA re	
c 18	33	100.0	732	2 AAV51396	AAv51396 UC pANCA	
c 19	33	100.0	753	4 AAF30632	Aaf30632 Anti-chel	
c 20	33	100.0	765	13 ADQ98099	Adq98099 Chimeric	

ALIGNMENTS

RESULT 1

ID ABN84084	Standard; DNA; 33 BP.
XX	
ID ABN84084;	
AC	
XX	
DT 23-SEP-2002 (first entry)	
XX	
DE Heavy chain CH1 constant region primer.	
XX	
Antibody; PRLS-CAT; vector; primer; SS.	
XX	
OS Unidentified.	
OS	
PN WO200246435-A2.	
XX	
PD 13-JUN-2002.	
XX	
PP 05-DEC-2001; 2001WO-US047452.	
XX	
PR 05-DEC-2000; 2000US-0251440P.	
XX	
PA (ALEX-) ALEXION PHARM INC.	
XX	
PA Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;	
PI McWhirter J;	
DR WPI; 2002-537569/57.	

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	33	100.0	33	6 ABN84084	Abn84084 Heavy cha	
c 2	33	100.0	59	6 ABN84085	Abn84085 Antibody	
c 3	33	100.0	681	13 ADQ98070	Adq98070 Chimeric	
c 4	33	100.0	681	13 ADQ98075	Adq98075 Chimeric	
c 5	33	100.0	681	13 ADQ98086	Adq98086 Chimeric	
c 6	7	33	100.0	681	13 ADQ98087	Adq98087 Chimeric
c 7	7	33	100.0	681	13 ADQ98088	Adq98088 Chimeric
c 8	33	100.0	681	13 ADQ98089	Adq98089 Chimeric	
c 9	33	100.0	687	2 AAT15202	Aat15202 pC3Ap313	
c 10	33	100.0	699	2 AAT86666	Aat86666 DNA encod	
c 11	33	100.0	699	2 AAT44088	Aat44088 Ulcerativ	
c 12	33	100.0	699	2 ADB5154	Adb5154 p-ANCA re	
c 13	33	100.0	699	2 AAV51394	AAv51394 UC pANCA	
c 14	33	100.0	699	2 AAX91122	Aax91122 NANUC-2 a	
c 15	33	100.0	699	2 AAZ90667	AAz90667 UC pANCA	
c 16	33	100.0	732	2 AAT44089	Aat44089 Ulcerativ	
c 17	33	100.0	732	2 ADB51516	Adb51516 p-ANCA re	
c 18	33	100.0	732	2 AAV51396	AAv51396 UC pANCA	
c 19	33	100.0	753	4 AAF30632	Aaf30632 Anti-chel	
c 20	33	100.0	765	13 ADQ98099	Adq98099 Chimeric	

The present sequence is a heavy chain CH1 constant region primer that is used in the engineering of plasmids of the invention, especially plasmid PRLS-CAT (see ABN84078), for the in situ production of genes. It was found nucleic acids encoding at least a portion of an antibody can be directly incorporated into a plasmid by reverse transcription of mRNA. The plasmid is engineered to contain 2 template annealing sequences and a restriction site located between the annealing sequences.

Claim 34; Page 19; 65pp; English.

The present sequence is a heavy chain CH1 constant region primer that is used in the engineering of plasmids of the invention, especially plasmid PRLS-CAT (see ABN84078), for the in situ production of genes. It was found nucleic acids encoding at least a portion of an antibody can be directly incorporated into a plasmid by reverse transcription of mRNA. The plasmid is engineered to contain 2 template annealing sequences and a restriction site located between the annealing sequences.

Claim 34; Page 19; 65pp; English.

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OM nucleic - nucleic search, using bw model

Run on: June 1, 2005, 16:29:42 ; Search time 823.336 Seconds

(without alignments)

1 ttgtcacaaatttgggttcttttgtc 33

1942.126 Million cell updates/sec

Title: US-10-006-591A-8

Perfect Score: 33

Sequence: 1 ttgtcacaaatttgggttcttttgtc 33

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708333 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:

9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

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 1: 9b_ba:*
 2: 9b_hdg:*
 3: 9b_in:*
 4: 9b_om:*
 5: 9b_ov:*
 6: 9b_pa:*
 7: 9b_ph:*
 8: 9b_pi:*
 9: 9b_pr:*
 10: 9b_ro:*
 11: 9b_sbs:*
 12: 9b_sy:*
 13: 9b_un:*
 14: 9b_v1:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	33	100.0	33	6	AX642156	AX642156 Sequence
c 2	33	100.0	59	6	AX642157	AX642157 Sequence
c 3	33	100.0	59	6	AX642158	AX642158 Sequence
c 4	33	100.0	687	6	AR105449	AR105449 Sequence
c 5	33	100.0	687	6	I65402	I65402 Sequence
c 6	33	100.0	699	6	AR051551	AR051551 Sequence
c 7	33	100.0	699	6	AR098121	AR098121 Sequence
c 8	33	100.0	699	6	AR300196	AR300196 Sequence
c 9	33	100.0	732	6	AR051552	AR051552 Sequence
c 10	33	100.0	1413	6	AX556349	AX556349 Sequence
c 11	33	100.0	1413	6	AX705448	AX705448 Sequence
c 12	33	100.0	1418	6	A49389	A49389 Sequence
c 13	33	100.0	1418	6	AR176296	AR176296 Sequence
c 14	33	100.0	1428	6	AR031184	AR031184 Sequence
c 15	33	100.0	1428	6	AR031186	AR031186 Sequence
c 16	33	100.0	1428	6	AR042589	AR042589 Sequence
c 17	33	100.0	1428	6	AR042581	AR042581 Sequence
c 18	33	100.0	1428	6	AR059282	AR059282 Sequence
c 19	33	100.0	1428	6	AR059284	AR059284 Sequence

ALIGNMENTS

```

RESULT 1
AX642156
LOCUS AX642156
DEFINITION Sequence 8 from Patent WO246435.
ACCESSION AX642156
VERSION AX642156.1
KEYWORDS GI:28474644
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bowdish, K.S., Barbas-Fredrickson, S., Lin, Y.C., Renshaw, M., Wild, M., and McWhirter, J.
TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0246135 A 8 13-JUN-2002;
FEATURES Location/Qualifiers 1. 33
Source
 1. 33
/organism="synthetic construct"
/mol type="unassigned DNA"
/db _xref="taxon:33630"
/note="Description for Artificial Sequence: primer"

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ORIGIN

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Query Match 100.0% Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 33; Conservative 0; N mismatches 0;
Indels 0; Gaps 0;
Qy 1 TTTGTCACAGATTTGGGCTCTGCTTCTTGTC 33
Db 1 TTTGTCACAGATTTGGGCTCTGCTTCTTGTC 33
RESULT 2
AX642157/c
LOCUS AX642157
DEFINITION Sequence 9 from Patent WO246435.
ACCESSION AX642157
VERSION AX642157.1
KEYWORDS GI:28474645
SOURCE synthetic construct
ORGANISM synthetic construct

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 183.866 Seconds

(without alignment)

668.687 Million cell updates/sec

Title: US-10-006-591A-7
Perfect score: 20

Sequence: 1 gactgaccaggctgnacctg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters:

11413164

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgm2_6/picodata/1/pubnpna/us07_PUBCOMB.seq:
 2: /cgm2_6/picodata/1/pubnpna/FCT_NEW_PUB.seq:
 3: /cgm2_6/picodata/1/pubnpna/us06_PUBCOMB.seq:
 4: /cgm2_6/picodata/1/pubnpna/us06_PUBCOMB.seq:
 5: /cgm2_6/picodata/1/pubnpna/us07_NEW_PUB.seq:
 6: /cgm2_6/picodata/1/pubnpna/PCTUS_PUBCOMB.seq:
 7: /cgm2_6/picodata/1/pubnpna/us08_NEW_PUB.seq:
 8: /cgm2_6/picodata/1/pubnpna/us08_PUBCOMB.seq:
 9: /cgm2_6/picodata/1/pubnpna/us09_PUBCOMB.seq:
 10: /cnr2_6/picodata/1/pubnpna/us09B_PUBCOMB.seq:
 11: /cnr2_6/picodata/1/pubnpna/us09C_PUBCOMB.seq:
 12: /cnr2_6/picodata/1/pubnpna/us09_NEW_PUB.seq:
 13: /cnr2_6/picodata/1/pubnpna/us10A_PUBCOMB.seq:
 14: /cnr2_6/picodata/1/pubnpna/us10_PUBCOMB.seq:
 15: /cnr2_6/picodata/1/pubnpna/us10C_PUBCOMB.seq:
 16: /cnr2_6/picodata/1/pubnpna/us10D_PUBCOMB.seq:
 17: /cnr2_6/picodata/1/pubnpna/us10F_PUBCOMB.seq:
 18: /cnr2_6/picodata/1/pubnpna/us10I_PUBCOMB.seq:
 19: /cnr2_6/picodata/1/pubnpna/us10I_NEW_PUB.seq:
 20: /cnr2_6/picodata/1/pubnpna/us11I_NEW_PUB.seq:
 21: /cnr2_6/picodata/1/pubnpna/us60I_NEW_PUB.seq:
 22: /cnr2_6/picodata/1/pubnpna/us60I_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	95.0	20	14	US-10-006-591-7
c 2	19	95.0	20	Sequence 7, Appl
c 3	19	95.0	20	Sequence 11, Appl
c 4	19	95.0	20	Sequence 17, Appl
c 5	19	95.0	20	Sequence 18, Appl
c 6	19	95.0	21	Sequence 19, Appl
c 7	19	95.0	21	Sequence 20, Appl
c 8	19	95.0	21	Sequence 21, Appl
c 9	19	95.0	21	Sequence 22, Appl
c 10	19	95.0	23	Sequence 23, Appl
c 11	19	95.0	23	Sequence 23, Appl

Sequence 12, Appl
Sequence 49, Appl
Sequence 7, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 121, APP
Sequence 38, Appl
Sequence 31, Appl
Sequence 28, Appl
Sequence 38, Appl
Sequence 58, Appl
Sequence 28, Appl
Sequence 23, Appl
Sequence 53, Appl
Sequence 40, Appl
Sequence 94, Appl
Sequence 105, APP
Sequence 54, APP
Sequence 28, APP
Sequence 33, APP
Sequence 12, APP
Sequence 272, APP
Sequence 41, APP
RESULT 1
; Sequence 7, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Reshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN
; FILE REFERENCE: 1087_3
; CURRENT APPLICATION NUMBER: US/10/006_591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NO: 14
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence. collar sequence

; NAME/KEY: misc_feature
; LOCATION: (15..(15)
; OTHER INFORMATION: n is c or a
; US-10-006-591-7
Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;

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 OM nucleic - nucleic search, using sw model
 Run on: June 1, 2005, 18:46:12 ; Search time 43.1933 Seconds
 (without alignments)
 .757.653 Million cell updates/sec

Title: US-10-006-591A-7
 Perfect score: 20
 Sequence: 1 gactggccaggctgnacacctg 20

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
 1: /cgm2_6/ptodata/1/ina/5A_COMB.seq:
 2: /cgm2_6/ptodata/1/ina/5B_COMB.seq:
 3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:
 4: /cgm2_6/ptodata/1/ina/6B_COMB.seq:
 5: /cgm2_6/ptodata/1/ina/PCTUS_COHB.seq:
 6: /cgm2_6/ptodata/1/ina/backfile1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	95.0		23	1 US-08-211-202-30	Sequence 30, APP1
C 2	95.0		23	1 US-08-307-619-10	Sequence 10, APP1
C 3	95.0		23	2 US-08-350-260A-56	Sequence 56, APP1
C 4	95.0		23	3 US-09-030-763-10	Sequence 10, APP1
C 5	95.0		23	4 US-09-104-337A-56	Sequence 56, APP1
C 6	95.0		23	4 US-10-067-443-33	Sequence 33, APP1
C 7	95.0		23	4 US-09-726-219A-81	Sequence 43, APP1
C 8	95.0		38	1 US-08-211-202-43	Sequence 2, APP1
C 9	95.0		43	4 US-09-456-030A-2	Sequence 2, APP1
C 10	95.0		43	4 US-09-513-234-2	Sequence 26, APP1
C 11	95.0		45	4 US-08-495-209-26	Sequence 26, APP1
C 12	95.0		45	5 PCT-US96-10805-26	Sequence 26, APP1
C 13	95.0		56	1 US-08-111-202-101	Sequence 16, APP1
C 14	95.0		56	1 US-08-307-619-16	Sequence 15, APP1
C 15	95.0		56	2 US-08-244-597-15	Sequence 62, APP1
C 16	95.0		56	2 US-08-50-260A-62	Sequence 16, APP1
C 17	95.0		56	3 US-09-050-783-16	Sequence 62, APP1
C 18	95.0		56	4 US-09-104-337A-62	Sequence 15, APP1
C 19	95.0		56	4 US-09-19-224-15	Sequence 15, APP1
C 20	95.0		56	4 US-09-19-722-15	Sequence 15, APP1
C 21	95.0		56	4 US-09-572-392A-15	Sequence 15, APP1
C 22	95.0		56	4 US-09-723-756-15	Sequence 15, APP1
C 23	95.0		56	4 US-09-332-840-15	Sequence 87, APP1
C 24	95.0		56	4 US-09-726-219A-87	Sequence 64, APP1
C 25	95.0		71	3 US-08-147-64	Sequence 61, APP1
C 26	95.0		78	1 US-08-477-877B-61	Sequence 61, APP1
C 27	95.0		78	1 US-08-472-281A-61	Sequence 61, APP1

ALIGNMENTS

RESULT 1
 US-08-211-202-30/C
 ; Sequence 30, Application US/08211202
 ; Patent No. 5565322
 / GENERAL INFORMATION:
 / APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
 / APPLICANT: BAER, Michael
 / APPLICANT: JESPERS, Laurent Stephane Anne Therese
 / APPLICANT: WINTER, Gregory Paul
 / TITLE OF INVENTION: Production of chimeric antibodies - a
 / TITLE OF INVENTION: combinatorial approach
 / NUMBER OF SEQUENCES: 144
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 ADDRESSEE: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 / MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/211-202
 / FILING DATE: 23-SEP-1992
 / CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: GB 9120252.3
 / FILING DATE: 23-SEP-1991
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: GB 9120377.8
 / FILING DATE: 25-SEP-1991
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: GB 9206318.9
 / FILING DATE: 24-MAR-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: GB 9206372.6
 / FILING DATE: 24-MAR-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: PCT/GB92/00883
 / FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 / NAME: David W. Clough
 / REGISTRATION NUMBER: 36,107
 / REFERENCE/DOCKET NUMBER: 28111/31960
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 312-474-6300

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 1225.04 Seconds
 (without alignments)

Title: US-10-006-591A-7
 Perfect score: 20

Sequence: 1 gactgcaccaaggctgnaccgt 20

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST*
 1: 9b_est1: *
 2: 9b_est2: *
 3: 9b_hnc: *
 4: 9b_est3: *
 5: 9b_est4: *
 6: 9b_est5: *
 7: 9b_est6: *
 8: 9b_gss1: *
 9: 9b_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	19	95.0	194	2	AW408784		AW408784 UI-HF-BMO
C 2	19	95.0	226	2	AW505280		AW505280 UI-HF-BNO
C 3	19	95.0	231	2	AW382578		AW382578 CM0-HT033
C 4	19	95.0	234	5	BQ84534		BQ84534 K-EST0149
C 5	19	95.0	238	7	T29670		T29670 EST89669 Hu
C 6	19	95.0	244	2	AW403100		AW403100 UI-HF-BKO
C 7	19	95.0	264	2	AW403511		AW403511 UI-HF-BKO
C 8	19	95.0	264	2	AA300571		AA300571 EST1361
C 9	19	95.0	282	8	B73518		B73518 C-T-HSP-857
C 10	19	95.0	300	1	AU098611		AU098611 AU098611
C 11	19	95.0	300	1	AU098624		AU098624 AU098624
C 12	19	95.0	302	2	AW403015		AW403015 UI-HF-BKO
C 13	19	95.0	302	2	AW607003		AW607003 RC3-HT044
C 14	19	95.0	305	2	AW402941		AW402941 UI-HF-BKO
C 15	19	95.0	306	2	AW402857		AW402857 UI-HF-BKO
C 16	19	95.0	306	2	AW403516		AW403516 UI-HF-BKO
C 17	19	95.0	312	2	AW401829		AW401829 UI-HF-BKO
C 18	19	95.0	321	2	AW130201		AW130201 xf29n05.X
C 19	19	95.0	331	2	AW407729		AW407729 UI-HF-BLO
C 20	19	95.0	341	2	BF128876		BF128876 601811064
C 21	19	95.0	344	2	AW403535		AW403535 UI-HF-BKO
C 22	19	95.0	359	2	BE010378		BE010378 CM0-BN018
C 23	19	95.0	364	2	AW380763		AW380763 CM4-HT028
C 24	19	95.0	381	4	BM798753		BM798753 K-EST0082

RESULT 1		ALIGNMENTS	
LOCUS	AW408784/C	DEFINITION	194 bp mRNA linear EST 16-FEB-2000
IMAGE	UI-HF-BMO-adx-b-10-0-UT.r1 NIH_MGC_38 Homo sapiens cDNA clone	VERSION	IMAGE:3063115 5', mRNA sequence.
ACCESSION	AW408784	VERSION	AW408784.1 GI:6927841
KEYWORDS	BST.	SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE	NIH-MGC http://mgc.ncbi.nih.gov/
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	JOURNAL	Unpublished (1999)
TITLE		COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-request.nih.gov
JOURNAL			Eco RI site shown at the beginning of the sequence.
COMMENT			Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
			CDNA Library Preparation: M.B. Soares Lab
			CDNA Library Arrayed by: M.B. Soares Lab
			DNA Sequencing by: M.B. Soares Lab
			Clone distribution: MGCG clone distribution information can be found through the I.M.A.G.E. Consortium/LINX at: www-bio-linn.genome.org/bcrp/image/image.html
			seq.primer: M13 Forward.
			FEATURES
			Source
			1..194
			/organism="Homo sapiens"
			/mol_type="mRNA"
			/db_xref="taxon:9606"
			/clone_lib="NIH_MGC_38"
			/notes="Vector: PNT3-Pac; Site 1: NotI; Site 2: Eco RI;
			Constructed from size fractionated cytoplasmic mRNA (2.5-3.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library Preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
			ORIGIN
			Query Match 95.0%; Score 19; DB 2; Length 194; Best local Similarity 95.0%; Pred. No. 4.8e+02;

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 147.731 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20

Sequence: 1.gactgcaccaggctgnacctg 20

Scoring table: IDENTITY_NUC
GapOp 10.0 , Gapext 1.0

Searched: 439026 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16bdec04:
 1: geneseqm1980s:
 2: geneseqm1990s:
 3: geneseqm2000s:
 4: geneseqm2001as:
 5: geneseqm2001bs:
 6: geneseqm2002as:
 7: geneseqm2002bs:
 8: geneseqm2003as:
 9: geneseqm2003bs:
 10: geneseqm2003bs:
 11: geneseqm2003bs:
 12: geneseqm2004as:
 13: geneseqm2004bs:
 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	19	95.0	20	6	ABN84083	Abs84083 FR1 collar
C 2	19	95.0	20	8	ACG44845	AcG44845 Human ant
C 3	19	95.0	20	12	AD039458	Ado39458 Novel hum
C 4	19	95.0	20	12	AD075790	Ado75790 Anti-IL-8
C 5	19	95.0	20	13	ADS88084	Ad888084 Human CD2
C 6	19	95.0	20	13	ADR6911	Adr6911 Human IL-
C 7	19	95.0	21	10	ADE03287	Ado03287 Human imm
C 8	19	95.0	22	2	AAQ62395	Aaq62395 Vector pV
C 9	19	95.0	23	2	AAQ32275	Aaq32275 Human hea
C 10	19	95.0	23	2	AAQ23700	Aaq23700 Primer hu
C 11	19	95.0	23	2	AAQ39333	Aaq39333 VH domain
C 12	19	95.0	23	2	AAQ48987	Aaq48987 Multimer
C 13	19	95.0	23	2	AAQ29177	Aaq29177 HuV1a 5'
C 14	19	95.0	23	2	AAZ24687	Aaz24687 Llana IgG
C 15	19	95.0	23	2	AAX76595	Aax76595 Human IgG
C 16	19	95.0	23	3	AAQ3843	Aaq3843 Human IgG
C 17	19	95.0	23	4	ABA03072	Aba03072 PCR prime
C 18	19	95.0	23	4	AAD20055	Aad20055 Human ant
C 19	19	95.0	23	4	AAD13300	Aad13300 Human VH
C 20	19	95.0	23	4	AAD13199	Aad13199 Human VH

ALIGNMENTS

RESULT 1						
ID	ABN84083	standard; DNA	20 BP.			
XX				AC	ABN84083;	
XX				XX		
XX				DT	23-SEP-2002 (first entry)	
XX				XX		
DE				DE	FR1_collar sequence.	
XX				XX		
XX				XX	Antibody; pRNU5-CAT; vector; primer; ss.	
OS				XX		
XX				XX	Unidentified.	
PN				XX	WO200246435-A2.	
XX				XX		
PD				XX	13-JUN-2002.	
XX				XX	PP 05-DEC-2001; 2001WO-US047452.	
PR				XX	05-DEC-2000; 2000US-051440P.	
XX				XX	WO200246435-A2.	
PA				XX	(ALEX-) ALEXION PHARM INC.	
XX				XX		
PI				PI	Boudish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;	
PI				PI	McWhirter J;	
XX				XX	WP; 2002-537569/57.	
PT				PT	Plasmid for in situ production of genes, comprises two template annealing sequences, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences.	
XX				XX	DR	
PS				PS	Claim 36; Page 19; 65pp; English.	
XX				XX	The present sequence is an antibody framework region 1 (FR1) collar oligonucleotide that is used in the engineering of plasmids of the invention, especially plasmid PR5-Ctr (see ABN84078), for the in situ production of genes. It was found nucleic acids encoding at least a portion of an antibody can be directly incorporated into a plasmid by reverse transcription of mRNA. The plasmid is engineered to contain 2 template annealing sequences, i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a	

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DM nucleic - nucleic search, using sw model
Run on: June 1, 2005, 16:29:42 ; **Search time** 498.992 Seconds
 (without alignments)
 1942.126 Million cell updates/sec
Title: US-10-006-591A-7
Perfect score: 20
Sequence: 1 gactccaccgtgnacctg 20
Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
Searched: 4708233 seqB, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0.8
Sequence:
 AX357136 Sequence
 AX376700 Sequence
 AX795212 Sequence
 A27204 Oligonucleic
 A33845 Synthetic
 AX658910 Sequence
 CO879714 Sequence
 CO879694 Sequence
 AX190443 Sequence
 AX657269 Sequence
 AR454042 Sequence
 E11299 PCR primer
 AX175350 Sequence
 AR243937 Sequence
 CO849429 Sequence
 AX004925 Sequence
 BD074255 Method
 AX376805 Sequence
 AX601773 Sequence
 A27390 Oligonucleic
 A32943 Synthetic
 A33903 Synthetic
 AR077347 Sequence

ALIGNMENT S

RESULT 1
 CQ874135/c
 LOCUS CQ874135 Sequence 11 from Patent wO2004076620.
 DEFINITION CQ874135
 ACCESSION CQ874135
 VERSION CQ874135.1 GI:512747700
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 van de Winkel,J.G., van Dijk,M.A., Schuurman,J.J., Gerritsen,A.F.,
 AUTHORS Baadsgaard,O.D. and Petersen,J.R.
 TITLE Human mtIbodies specific for interleukin 15 (il-15)
 JOURNAL Patent: WO 2004076620-A 11 10-SEP-2004;
 GENMAB A/S (DK)
 FEATURES Location/Qualifier
 source 1. 20.
 /organism="Homo sapiens"
 /mol="rRNA-mtDNA
 summaries
 * the number of results predicted by chance to have a
 higher than or equal to the score of the result being printed,
 derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
					DB	
c	1	19	95.0	20	6	CQ874135 Sequence
c	2	19	95.0	20	6	AK644155 Sequence
c	3	19	95.0	21	6	AX740283 Sequence
c	4	19	95.0	22	6	A38157 Sequence 1
c	5	19	95.0	23	6	A27195 Oligonucleo
c	6	19	95.0	23	6	A32937 Synthetic P
c	7	19	95.0	23	6	A33832 Synthetic P
c	8	19	95.0	23	6	AR07341 Sequence
c	9	19	95.0	23	6	AR117961 Sequence
c	10	19	95.0	23	6	BD231855 Methods f
c	11	19	95.0	23	6	CQB46560 Sequence
c	12	19	95.0	23	6	E09108 Synthetic o
c	13	19	95.0	23	6	I27516 Sequence 30
c	14	19	95.0	23	6	I195612 Sequence 10
c	15	19	95.0	23	6	AR265404 Sequence
c	16	19	95.0	23	6	AR310925 Sequence
c	17	19	95.0	23	6	AR428815 Sequence
c	18	19	95.0	23	6	AR432217 Sequence
c	19	19	95.0	23	6	AV00542 Sequence

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OM nucleic - nucleic search, using SW model

Run on: June 1, 2005, 20:13:07 ; Search time 459.664 Seconds
 (without alignments)
 Perfect score: 668.687 Million cell updates/sec

Title: US-10-006-591A-4
 Sequence: 1 attaaactctccctgttg.....tgacggcgaaacctaggccc 50

Scoring table: IDENTITY NUC
 GapP: 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgns_6/ptodata/1/pub/pna/us07_PUBCOMB.seq;*
 2: /cgns_6/ptodata/1/pub/pna/PCT_NSW_PUB.seq;*
 3: /cgns_6/ptodata/1/pub/pna/us06_NEW_PUB.seq;*
 4: /cgns_6/ptodata/1/pub/pna/us05_PUBCOMB.seq;*
 5: /cgns_6/ptodata/1/pub/pna/us07_NEW_PUB.seq;*
 6: /cgns_6/ptodata/1/pub/pna/PCTNS_PUBCOMB.seq;*
 7: /cgns_6/ptodata/1/pub/pna/us08_NEW_PUB.seq;*
 8: /cgns_6/ptodata/1/pub/pna/us09_PUBCOMB.seq;*
 9: /cgns_6/ptodata/1/pub/pna/us09A_PUBCOMB.seq;*
 10: /cgns_6/ptodata/1/pub/pna/us09B_PUBCOMB.seq;*
 11: /cgns_6/ptodata/1/pub/pna/us09C_PUBCOMB.seq;*
 12: /cgns_6/ptodata/1/pub/pna/us09_NSW_PUB.seq;*
 13: /cgns_6/ptodata/1/pub/pna/us10_PUBCOMB.seq;*
 14: /cgns_6/ptodata/1/pub/pna/us10_NEW_PUB.seq;*
 15: /cgns_6/ptodata/1/pub/pna/us10C_PUBCOMB.seq;*
 16: /cgns_6/ptodata/1/pub/pna/us10D_PUBCOMB.seq;*
 17: /cgns_6/ptodata/1/pub/pna/us10F_PUBCOMB.seq;*
 18: /cgns_6/ptodata/1/pub/pna/us10I_PUBCOMB.seq;*
 19: /cgns_6/ptodata/1/pub/pna/us10_NEW_PUB.seq;*
 20: /cgns_6/ptodata/1/pub/pna/us11_NEW_PUB.seq;*
 21: /cgns_6/ptodata/1/pub/pna/us60_NEW_PUB.seq;*
 22: /cgns_6/ptodata/1/pub/pna/us60_PUBCOMB.seq;*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	50	100.0	50	14	US-10-006-591-4
C 2	50	100.0	68	14	US-10-006-591-5
C 3	50	100.0	76	14	US-10-006-591-6
C 4	50	100.0	357	9	US-09-910-059-16
C 5	50	100.0	729	16	US-10-016-986-152
C 6	50	100.0	729	16	US-10-016-986-168
C 7	50	100.0	729	17	US-10-016-907-1
C 8	50	100.0	1539	18	US-10-492-729-4
C 9	50	100.0	1539	18	US-10-492-729-12
C 10	48.4	96.8	724	9	US-09-237-061-1
C 11	48.4	96.8	1081	9	US-09-746-359A-20

ALIGNMENTS

RESULT 1
 US-10-006-591-4

; Sequence 4, Application US/10006591
 ; Publication No. US20030049731A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bowditch, Katherine S.
 ; APPLICANT: Frederickson, Shana
 ; APPLICANT: Lin, Ying-Chi
 ; APPLICANT: Renshaw, Mark
 ; APPLICANT: Wild, Martha
 ; APPLICANT: McWhirter, John
 ; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GBN
 ; FILE REFERENCE: 1087-3
 ; CURRENT APPLICATION NUMBER: US/10/006,591
 ; CURRENT FILING DATE: 2001-12-05
 ; PRIOR APPLICATION NUMBER: 60/251,440
 ; PRIOR FILING DATE: 2000-12-05
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 US-10-006-591-4

Query Match Similarity 100.0%; Score 50; DB 14; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 50; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 ATTACACTCTCCCTGTTGAGCTCTTGTGAGGGCGAACCTAGGCC 50
 Db 1 ATTACACTCTCCCTGTTGAGCTCTTGTGAGGGCGAACCTAGGCC 50

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 107.983 Seconds
(without alignments)

757.653 Million cell updates/sec

Title: US-10-006-591A-4

Perfect score: 50

Sequence:

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1 attaacacttccctgttg.....tgacggcgaaactcaggccc 50
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 24055568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6_ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6_ptodata/1/ina/5B_COMB.seq:
3: /cgn2_6_ptodata/1/ina/6A_COMB.seq:
4: /cgn2_6_ptodata/1/ina/6B_COMB.seq:
5: /cgn2_6_ptodata/1/ina/backf1seq:
6: /cgn2_6_ptodata/1/ina/backf1seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
C 1	50	100.0	357	3	US-09-171-945-46	Sequence 46, App1
C 2	50	100.0	646	1	US-08-300-386A-2	Sequence 2, App1
C 3	50	100.0	646	3	US-08-931-645-2	Sequence 2, App1
C 4	50	100.0	646	5	PCT-US94-01258-2	Sequence 2, App1
C 5	50	100.0	646	5	PCT-US95-11235-2	Sequence 2, App1
C 6	50	100.0	729	1	US-08-276-852-152	Sequence 152, App
C 7	50	100.0	729	1	US-08-276-852-168	Sequence 168, App
C 8	50	100.0	729	1	US-08-899-575-152	Sequence 152, App
C 9	50	100.0	729	1	US-08-899-575-168	Sequence 168, App
C 10	50	100.0	729	1	US-08-899-575-152	Sequence 152, App
C 11	50	100.0	729	1	US-08-899-575-168	Sequence 168, App
C 12	50	100.0	729	5	PCT-US95-08743-152	Sequence 152, App
C 13	50	100.0	729	2	PCT-US95-08743-168	Sequence 168, App
C 14	50	100.0	732	2	US-08-860-882A-29	Sequence 29, App1
C 15	50	100.0	732	3	US-08-011-769A-26	Sequence 26, App1
C 16	50	100.0	3217	3	US-08-423-439-32	Sequence 52, App1
C 17	50	100.0	4691	3	US-08-591-632-43	Sequence 43, App1
C 18	50	100.0	4691	3	US-09-611-451-43	Sequence 43, App1
C 19	50	100.0	6166	3	US-08-591-632-51	Sequence 51, App1
C 20	48.4	96.8	6166	3	US-09-611-451-51	Sequence 51, App1
C 21	48.4	96.8	724	4	US-09-237-061-1	Sequence 1, App1
C 22	48.4	96.8	1081	4	US-09-746-359A-20	Sequence 20, App1
C 23	48.4	96.8	5703	1	US-08-467-420A-50	Sequence 50, App1
C 24	48.4	96.8	5703	1	US-08-470-110A-50	Sequence 50, App1
C 25	48.4	96.8	5703	1	US-08-667-769A-50	Sequence 50, App1
C 26	48.4	96.8	5703	2	US-08-940-371-50	Sequence 50, App1
C 27	48.4	96.8	5703	3	US-08-637-647-50	Sequence 50, App1

ALIGNMENTS

RESULT 1
US-09-171-945-46/C
Sequence 46, Application US/09171945
; Patent No. 62277599

; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; COPILEY, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Monoclonal Antibody to CEA, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT FILING DATE: 1998-10-29
; PRIORITY NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIORITY NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIORITY NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-46

Qy 1 ATTAACACTCCCTGTTGAGCTCTTGTGAACTCTAGGCC 50
Db 343 ATTAACACTCCCTGTTGAGCTCTTGTGAACTCTAGGCC 294

RESULT 2
US-08-100-396A-2/C
Sequence 2, Application US/08300386A
; Patent No. 5667988

; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Richard A
; APPLICANT: Lerner, Dennis R
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 3062.6 Seconds
 (without alignments)
 621.436 Million cell updates/sec

Title: US-10-006-591A-4

Perfect score: 50
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Scoring table: IDENTITY_NUC
 Gapop_10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gbb1:*

9: gb_gbb2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
c 1	48	96.0	246	BE828579 CM1-ET0043
c 2	48	96.0	275	BE182590 RC3-BT064
c 3	47.4	94.8	291	AW131435 xf63e02.X
c 4	47.4	94.8	291	AW512732 xo08e12.X
c 5	47.4	94.8	296	AI950761 wx5903.X
c 6	47.4	94.8	299	AA933587 om61h09.X
c 7	47.4	94.8	310	AW188933 xk9e12.X
c 8	47.4	94.8	314	AI620130 tu9b07.X
c 9	47.4	94.8	325	AI682755 wc61h05.X
c 10	47.4	94.8	367	BF74509 MYE1290a
c 11	47.4	94.8	796	CB938668 AGENCOURT
c 12	47.4	94.8	810	CB956774 AGENCOURT
c 13	47.4	94.8	888	BQ881840 AGENCOURT
c 14	47.4	94.8	896	BQ884775 AGENCOURT
c 15	47.4	94.8	903	BQ708644 AGENCOURT
c 16	47.4	94.8	913	BQ711070 AGENCOURT
c 17	47.4	94.8	917	BQ711815 AGENCOURT
c 18	47.4	94.8	923	BQ709196 AGENCOURT
c 19	47.4	94.8	925	BQ707105 AGENCOURT
c 20	47.4	94.8	928	BQ709024 AGENCOURT
c 21	47.4	94.8	931	BQ701407 AGENCOURT
c 22	47.4	94.8	964	BQ705786 AGENCOURT
c 23	47.4	94.8	974	BQ707037 AGENCOURT
c 24	47.4	94.8	978	BQ059857 AGENCOURT

RESULT 1
 BE828579
 LOCUS BE828579 CM1-ET0043-030600-245-h04 Homo sapiens CDNA, mRNA sequence.

DEFINITION BE828579 EST
 ACCESSION BE828579
 VERSION 1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 TAXONID 9606
 ORGANISMS Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 246)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verloverski-Almeida,S., Briones,M.R., Naga1,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,P.F., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNALID 20202663
 MEDLINEID 10737800
 PUBLISHED COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics Ludwig Institute for Cancer Research,
 Brazil Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: absimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-CM1-ET0043-0106-245-h06&t4=1>)
 seq.primer: puc 18 forward
 High quality sequence start: 6
 High quality sequence stop: 246.

FEATURES Source
 1. Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="Adult"
 /clone lib="ET0043"
 /note="Organ: lung tumor; Vector: pucl8; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 369.328 Seconds

(without alignments)

801.421 Million cell updates/sec

Title: US-10-006-591A-4

Perfect score: 50
Sequence: 5' attaaacactccctgttg.....tgacgggaaactccaggccc 50

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390266 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:
 1: Geneseqn19008;*
 2: Geneseqn19008;*
 3: Geneseqn20008;*
 4: Geneseqn2001as;*
 5: Geneseqn2001bs;*
 6: Geneseqn2002as;*
 7: Geneseqn2002bs;*
 8: Geneseqn2003as;*
 9: Geneseqn2003bs;*
 10: Geneseqn2003cs;*
 11: Geneseqn2003ds;*
 12: Geneseqn2004as;*
 13: Geneseqn2004bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	50	100.0	50	6 ABN84080	Abn84080 Kappa con
C 2	50	100.0	68	6 ABN84081	Abn84081 Antibody
C 3	50	100.0	357	2 AAV17387	Aav17287 Human lig
C 4	50	100.0	357	2 AAX78043	Aax78043 Human ant
C 5	50	100.0	646	2 ARQ70487	Aaq70487 Anti-teta
C 6	50	100.0	646	2 AAT15203	Aat15203 PC3AP313
C 7	50	100.0	729	2 AAT40913	Aat40913 DNA encod
C 8	50	100.0	729	3 AAA32149	Aaa32149 Modified
C 9	50	100.0	729	3 AAA32163	Aaa32163 B12 IgG1
C 10	50	100.0	729	3 AAA31023	Aaa31023 Modified
C 11	50	100.0	729	3 AAA31037	Aaa31037 B12 IgG1
C 12	50	100.0	729	10 ADE06731	Ade06731 Human IgG
C 13	50	100.0	732	2 AAT42510	Aat42510 Humanised
C 14	50	100.0	1440	10 ADD24475	Add24475 Phagemid
C 15	50	100.0	1539	8 ADD56202	Add56202 X5 antibo
C 16	50	100.0	1539	8 ADD56203	Add56203 X5 antibo
C 17	50	100.0	2186	10 ADD6469	Add6469 Phagemid
C 18	50	100.0	2790	10 ADD6467	Add6467 Phagemid
C 19	50	100.0	2810	10 ADD6471	Add6471 Phagemid
C 20	50	100.0	3217	2 AAV72076	Aav72076 IRES-base

		c 21	50	100.0	4691	2 AA092546
		c 22	50	100.0	6166	2 AA092547
		c 23	49	98.0	663	12 AD006855
		c 24	49	98.0	663	12 AD006857
		c 25	48.4	96.8	724	2 AAX90423
		c 26	48.4	96.8	1081	4 AAH22820
		c 27	48.4	96.8	1081	5 AAS07648
		c 28	48.4	96.8	1081	6 ABK96181
		c 29	48.4	96.8	1081	6 ADD37589
		c 30	48.4	96.8	1081	6 ADD46567
		c 31	48.4	96.8	1081	12 ADJ83300
		c 32	48.4	96.8	2700	10 ABZ82071
		c 33	48.4	96.8	3000	12 AD014135
		c 34	48.4	96.8	3000	12 AD014138
		c 35	48.4	96.8	3100	10 ABZ82072
		c 36	48.4	96.8	3242	12 AD014124
		c 37	48.4	96.8	3255	12 AD014130
		c 38	48.4	96.8	3300	6 ABN86646
		c 39	48.4	96.8	3300	6 ABN86645
		c 40	48.4	96.8	3300	12 AD014127
		c 41	48.4	96.8	3300	12 AD014121
		c 42	48.4	96.8	3300	13 ADQ90708
		c 43	48.4	96.8	3300	13 ADQ90720
		c 44	48.4	96.8	3300	13 ADQ90702
		c 45	48.4	96.8	3300	13 ADQ90704

ALIGNMENTS

RESULT 1					
ABN84080					
ID ABN84080 standard; DNA; 50 BP.					
XX					
ABN84080;					
AC					
XX					
DT 23-SEP-2002 (first entry)					
XX					
DE Kappa constant region primer.					
XX					
KW Antibody; PRL5-CAT; vector; primer; ss.					
XX					
OS Unidentified.					
XX					
PW WO200246435-A2.					
XX					
PD 13-JUN-2002.					
XX					
PP 05-DEC-2001; 20001WO-US047452.					
XX					
PR 05-DEC-2000; 20000US-021440P.					
XX					
(ALEX-) ALEXION PHARM INC.					
PA					
PI Bowdish KS,					
MCwhirter J,					
DR					
XX					
WP1; 2002-537569/57.					
XX					
PT Plasmid for in situ production of genes, comprises two template annealing sequences, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences.					
PT					
PT restriction site located between the annealing sequences.					
PS Claim 33; Page 18; 65pp; English.					
XX					
CC The present invention is an antibody kappa constant region primer that is used in the engineering of plasmids of the invention, especially plasmid pR55-CAT (see ABN84078), for the in situ production of genes. It was found nucleic acids encoding at least a portion of an antibody can be directly incorporated into a plasmid by reverse transcribing of mRNA.					
CC The plasmid is engineered to contain 2 template annealing sequences, i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a portion of an antibody, and an					

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 1247.48 Seconds
(without alignments)

Title: US-10-006-591A-4

Perfect score: 50

Sequence: 1 attaaacactcccccgttg.....tgacggggaaaccttggcc 50

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 94164666

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba: *
2: gb_itg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pi: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	50	100.0	50	6	AX642152		AX642152 Sequence
c 2	50	100.0	68	6	AX641153		AX641153 Sequence
c 3	50	100.0	76	6	AX642154		AX642154 Sequence
c 4	50	100.0	357	6	A67220		A67220 Sequence 46
c 5	50	100.0	357	6	A94775		A94775 Sequence 19
c 6	50	100.0	634	9	AJ810487		AJ810487 Macaca fa
c 7	50	100.0	646	6	ARI05450		ARI05450 Sequence
c 8	50	100.0	646	6	I65403		I65403 Sequence 2
c 9	50	100.0	729	6	AR038305		AR038305 Sequence
c 10	50	100.0	729	6	AR038319		AR038319 Sequence
c 11	50	100.0	729	6	I58594		I58594 Sequence 15
c 12	50	100.0	729	6	I58608		I58608 Sequence 16
c 13	50	100.0	732	6	A51868		A51868 Sequence 32
c 14	50	100.0	1442	6	AR085834		AR085834 Sequence
c 15	50	100.0	2186	6	AJ744010		AJ744010 Sequence
c 16	50	100.0	2790	6	AJ744002		AJ744002 Sequence
c 17	50	100.0	2810	6	AJ744006		AJ744006 Sequence
c 18	50	100.0	3217	6	A83232		A83232 Sequence 52

ALIGNMENTS

RESULT 1
AX642152

LOCUS AX642152 Sequence 4 from Patent WO0246435.

DEFINITION AX642152 Version AX642152.1 GI:28476440

VERSION AX642152.1

KEYWORDS SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Bowdish,K.S., Barbas-Frederickson,S., Lin,Y.C., Renshaw,M., Wild,M.
and McWhirter,J.

TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0244435-A 4 JUN 2002;
ALEXION PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
Source 1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

ORIGIN

Query Match 100.0%; Score 50; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATTAACACTCTCCCTGTTGAGCTCTTGTGACGGCGAACCTAGGCC 50
Db 1 ATTAACACTCTCCCTGTTGAGCTCTTGTGACGGCGAACCTAGGCC 50

RESULT 2
AX642153 /C

LOCUS AX642153 Sequence 5 from Patent WO0246435.

DEFINITION AX642153 Version AX642153.1 GI:28476441

VERSION AX642153.1

KEYWORDS SOURCE synthetic construct
ORGANISM synthetic construct

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OM nucleic - nucleic search, using sw_model

Run on: June 1, 2005, 20:13:07 ; Search time 147.092 Seconds
 (without alignments)
 668.687 Million cell updates/sec

Title: US-10-006-591a-3
 Perfect score: 16

Sequence: 1_99gtcatctggatgt 16

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Published Applications NA:

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  2: /cgcn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq*
  3: /cgcn2_6/ptodata/1/pubnpa/us06_NEW_PUB.seq*
  4: /cgcn2_6/ptodata/1/pubnpa/us06_PUBCOMB.seq*
  5: /cgcn2_6/ptodata/1/pubnpa/PCTUS_PUBCOMB.seq*
  6: /cgcn2_6/ptodata/1/pubnpa/us08_NEW_PUB.seq*
  7: /cgcn2_6/ptodata/1/pubnpa/us08_PUBCOMB.seq*
  8: /cgcn2_6/ptodata/1/pubnpa/us09_PUBCOMB.seq*
  9: /cgcn2_6/ptodata/1/pubnpa/us09_PUBCOMB.seq*
  10: /cgcn2_6/ptodata/1/pubnpa/us09E_PUBCOMB.seq*
  11: /cgcn2_6/ptodata/1/pubnpa/us09C_PUBCOMB.seq*
  12: /cgcn2_6/ptodata/1/pubnpa/us09_NEW_PUB.seq*
  13: /cgcn2_6/ptodata/1/pubnpa/us10_PUBCOMB.seq*
  14: /cgcn2_6/ptodata/1/pubnpa/us10B_PUBCOMB.seq*
  15: /cgcn2_6/ptodata/1/pubnpa/us10C_PUBCOMB.seq*
  16: /cgcn2_6/ptodata/1/pubnpa/us10D_PUBCOMB.seq*
  17: /cgcn2_6/ptodata/1/pubnpa/us10F_PUBCOMB.seq*
  18: /cgcn2_6/ptodata/1/pubnpa/us10I_PUBCOMB.seq*
  19: /cgcn2_6/ptodata/1/pubnpa/us10L_NEW_PUB.seq*
  20: /cgcn2_6/ptodata/1/pubnpa/us11_NEW_PUB.seq*
  21: /cgcn2_6/ptodata/1/pubnpa/us16G_NEW_PUB.seq*
  22: /cgcn2_6/ptodata/1/pubnpa/us50_PUBCOMB.seq*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	93.8	16	US-10-006-591-3	Sequence 3, Appl
c 2	15	93.8	20	9 US-09-192-054-187	Sequence 187, App
c 3	15	93.8	20	9 US-09-192-854-199	Sequence 199, App
c 4	15	93.8	20	9 US-09-968-561A-325	Sequence 325, App
c 5	15	93.8	20	9 US-09-968-561A-337	Sequence 337, App
c 6	15	93.8	20	10 US-09-968-744A-325	Sequence 325, App
c 7	15	93.8	20	10 US-09-968-744R-337	Sequence 337, App
c 8	15	93.8	20	11 US-09-968-561A-325	Sequence 325, App
c 9	15	93.8	20	11 US-09-968-561A-337	Sequence 337, App
c 10	15	93.8	21	9 US-09-810-999-1	Sequence 1, Appl
c 11	15	93.8	21	10 US-09-389-565-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-10-006-591-3
; Sequence 3, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
;   APPLICANT: Bowdish, Katherine S.
;   APPLICANT: Frederickson, Shana
;   APPLICANT: Lin, Ying-Chi
;   APPLICANT: Renshaw, Mark
;   APPLICANT: Wild, Martha
;   APPLICANT: McWhirter, John
;   TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN
;   FILE REFERENCE: 1087.3
;   CURRENT APPLICATION NUMBER: US/10/006,591
;   CURRENT FILING DATE: 2001-12-05
;   PRIOR APPLICATION NUMBER: 60/251,440
;   PRIORITY FILING DATE: 2000-12-05
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: collar sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is c or t
US-10-006-591-3
Query Match 93.8%; Score 15; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 34.5546 Seconds

(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 gggtcatctggatgt 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 120284 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:

2405568

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgm2_6/pcodata/1/inia/5B_COMB.seq:
3: /cgm2_6/pcodata/1/inia/6A_COMB.seq:
4: /cgm2_6/pcodata/1/inia/6B_COMB.seq:
5: /cgm2_6/pcodata/1/inia/PCTUS_COMB.seq:
6: /cgm2_6/pcodata/1/inia/backf1les1.seq:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
c 1	15	93.8	18	1	US-08-307-619-33		Sequence 33, App1
c 2	15	93.8	18	2	US-08-350-260A-79		Sequence 79, App1
c 3	15	93.8	18	3	US-09-050-78-33		Sequence 33, App1
c 4	15	93.8	18	4	US-09-104-337A-79		Sequence 79, App1
c 5	15	93.8	20	4	US-09-192-054-187		Sequence 187, App1
c 6	15	93.8	20	4	US-09-192-054-199		Sequence 199, App1
c 7	15	93.8	21	3	US-08-84-3-109-7		Sequence 7, App1
c 8	15	93.8	21	4	US-09-380-084A-2		Sequence 2, App1
c 9	15	93.8	23	1	US-08-211-202-72		Sequence 72, App1
c 10	15	93.8	23	1	US-08-388-672A-14		Sequence 14, App1
c 11	15	93.8	23	3	US-09-080-054-14		Sequence 14, App1
c 12	15	93.8	23	3	US-09-672-009-31		Sequence 31, App1
c 13	15	93.8	23	3	US-09-025-203-29		Sequence 29, App1
c 14	15	93.8	23	3	US-09-025-403A-31		Sequence 31, App1
c 15	15	93.8	23	4	US-10-067-443-43		Sequence 43, App1
c 16	15	93.8	23	4	US-09-999-021-29		Sequence 29, App1
c 17	15	93.8	23	4	US-09-999-025-29		Sequence 29, App1
c 18	15	93.8	23	4	US-10-040-097-29		Sequence 29, App1
c 19	15	93.8	23	4	US-09-999-040-29		Sequence 29, App1
c 20	15	93.8	23	4	US-09-998-817-29		Sequence 29, App1
c 21	15	93.8	23	4	US-09-726-219A-99		Sequence 99, App1
c 22	15	93.8	24	4	US-09-726-219A-59		Sequence 59, App1
c 23	15	93.8	28	4	US-09-726-219A-58		Sequence 58, App1
c 24	15	93.8	31	4	US-08-407-620A-39		Sequence 39, App1
c 25	15	93.8	32	4	US-08-454-899G-64		Sequence 64, App1
c 26	15	93.8	32	4	US-08-454-899G-65		Sequence 65, App1
c 27	15	93.8	32	4	US-09-726-219A-139		Sequence 13, App1

ALIGNMENTS

RESULT 1	US-08-307-619-33/c	Sequence 33, Application US/08307619
	; Patent No. 573373	
	; GENERAL INFORMATION:	
	; APPLICANT: Johnson, Kevin S	
	; APPLICANT: Winter, Gregory P	
	; APPLICANT: Griffiths, Andrew D	
	; APPLICANT: Smith, Andrew JH	
	; APPLICANT: Waterhouse, P	
	; TITLE OF INVENTION: Methods for producing members of specific	
	; NUMBER OF SEQUENCES: 67	
	; CORRESPONDENCE ADDRESS:	
	; STREET: 600 Sears Tower, 233 South Wacker Drive	
	; CITY: Chicago	
	; STATE: Illinois	
	; COUNTRY: USA	
	; COMPUTER READABLES FORM:	
	; MEDIUM TYPE: floppy disk	
	; COMPUTER: IBM PC compatible	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/08/307,619	
	; FILING DATE: 16-SEP-1994	
	; CLASSIFICATION: 435	
	; CLASSIFICATION: GOIN 33/531, GOIN 33/68	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: PCT/GB93/00605	
	; FILING DATE: 24-MAR-1993	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: GB 9206318.9	
	; FILING DATE: 24-MAR-1992	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: PCT/GB92/00883	
	; FILING DATE: 15-MAY-1992	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: David W. Clough	
	; REGISTRATION NUMBER: 36,107	
	; REFERENCE/DOCKET NUMBER: 28111/32238	
	; TELECOMMUNICATION INFORMATION:	
	; TELEPHONE: 312-474-6300	
	; INFORMATION FOR SEQ ID NO: 33:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 18 base pairs	
	; TYPE: nucleic acid	
	; STRANDEDNESS: single	
	; TOPOLOGY: linear	

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 980.034 Seconds
(without alignments)
621,436 Million cell updates/sec

Title: US-10-006-591A-3

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0⁴
Maximum Match 100⁴
Listing First 45 summaries

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6: 9b_est5:*
7: 9b_est6:*
8: 9b_gbb1:*
9: 9b_gbb2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	15	93.8	133	2 AW405292 UI-HF-BLO	
C 3	15	93.8	141	2 AW408334 UI-HF-BLO	
C 4	15	93.8	142	6 CD692332 EST8855 h	
C 5	15	93.8	142	6 CD685432 EST1952 h	
C 6	15	93.8	143	6 CD690397 EST920 h	
C 7	15	93.8	159	7 CV317632 CM2-ET012	
C 8	15	93.8	160	2 AW610222 RC2-ST030	
C 9	15	93.8	166	4 BM828867 K-EST0099	
C 10	15	93.8	183	2 AW405083 UI-HF-BLO	
C 11	15	93.8	184	6 CA946304 nioh03.x	
C 12	15	93.8	186	6 CD704655	
C 13	15	93.8	188	6 CD707547 EST14074	
C 14	15	93.8	193	6 CB98288 AGENCOURT	
C 15	15	93.8	195	1 AA295576 EST1182	
C 16	15	93.8	202	2 AW407426 UI-HF-BLO	
C 17	15	93.8	202	6 CD710370 EST56897	
C 18	15	93.8	203	1 AA295622 EST10796	
C 19	15	93.8	203	1 CD704895 EST1422	
C 20	15	93.8	205	1 AA360654 EST1422	
C 21	15	93.8	208	2 AW407280 UI-HF-BLO	
C 22	15	93.8	208	6 CD692881 EST404 h	
C 23	15	93.8	208	6 CD708211 EST14738	
C 24	15	93.8	212	6 CD707121 EST3648 h	

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	CD708823 EST25390
	BB841882 MRI-ST009
	AA327437 EST30844
	BF876806 QVZ-ET010
	CD69881 EST6404 h
	AW405289 UI-HF-BLO
	AW404355 UI-HF-BLO
	AW407923 UI-HF-BLO
	AW406058 UI-HF-BLO
	BM825674 K-EST0097
	BE720151 RC3-HT088
	CD705199 EST21726
	BM825712 K-EST0097
	CD701383 EST17907
	CD70753 EST23980
	AQ629914 RPI-11-4
	BQ083770 K-BST046
	CD708395 EST25122
	BM826662 K-EST0099
	CD686563 EST3484 h

ALIGNMENTS

RESULT 1	CD704171/c	LOCUS	CD704171 EST20698	mRNA	linear	EST 25-JUN-2003
		DEFINITION	human nasopharynx	Homo sapiens	cDNA, mRNA sequence.	
		ACCESSION	CD704171			
		VERSION	CD704171.1	GI:32234801		
		KEYWORDS				
		SOURCE	Homo sapiens			
		ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Butteleostomi; Lukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo. Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.			
		REFERENCE	1 (bases 1 to 131)	Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.		
		AUTHORS				
		TITLE		Transcriptional Gene Expression Profile of Human Nasopharynx		
		JOURNAL		unpublished (2003)		
		COMMENT		Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 DongFeng Road East, GuangZhou 510060, China		
		FEATURES				
		SOURCE				
			1. .131	organism="Homo sapiens"		
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				/db_xref="taxon:9506"		
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				/clone_lib="human nasopharynx"		
				/note="ESTs generated from a normal nasopharynx cDNA library from Southern Chinese"		
		ORIGIN				
				Query Match 93.8%; Score 15; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy			1 GGCTCATCTGGATGT			
Db			101 GGCTCATCTGGATGT			

RESULT 2	AW405232/c	LOCUS	AW405292	mRNA	linear	EST 16-FEB-2000
				NTH_MGC_37 Homo sapiens	cdna clone	

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 118.185 Seconds
(without alignments)

801.421 Million cell updates/sec

Title: US-10-006-591A-3

Perfect score: 16

Sequence: 1 99gtcatctggatgt 16

Scoring table: IDNITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
Maximum Match 100\$

Listing first 45 summaries

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8: geneseqn2003as:*

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10: geneseqn2001cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	93.8	16	ABN84079		Abn84079 FR1 collar
C 2	15	93.8	18	2	AAO45011	Aad49011 Multimer
C 3	15	93.8	20	2	AAK33949	Aad35949 5' primer
C 4	15	93.8	20	2	AAK35937	Aad35937 5' primer
C 5	15	93.8	21	2	AAT38487	Aaa38487 Primer P1
C 6	15	93.8	21	2	AAV48233	Aav48233 Primer P1
C 7	15	93.8	21	3	AAZ47090	Aaz47090 Primer P1
C 8	15	93.8	21	3	Aaa91851	Aaa91851 Primer P1
C 9	15	93.8	21	6	ABK13448	Abk13448 Antibody
C 10	15	93.8	21	10	ADB03323	Ade03323 Human imm
C 11	15	93.8	21	10	ADB03324	Ade03324 Human imm
C 12	15	93.8	21	10	ADL53087	Adl53087 Chimeric
C 13	15	93.8	22	8	ACA6812	Aca6812 Hamster a
C 14	15	93.8	23	2	AAQ032314	Aaq032314 HUVCLaBAC
C 15	15	93.8	23	2	AAQ32718	Aaq32718 Primer Hu
C 16	15	93.8	23	2	AAQ33718	Aaq33718 Kappa-cha
C 17	15	93.8	23	2	AAQ62405	Aaq62405 Vector pV
C 18	15	93.8	23	2	AAZ2183	Aaz2183 Huvila ka
C 19	15	93.8	23	2	AAZ20999	Aaz20999 Humanised
C 20	15	93.8	23	2	AAZ76629	Aaz76629 Human sPV

ALIGNMENTS

C 21	15	93.8	23	4	ABA03082	PCR prime
C 22	15	93.8	23	4	AAD2029	Human int
C 23	15	93.8	23	4	AAD13310	Aadi3310 Human VL
C 24	15	93.8	23	4	AAD13209	Aadi3209 Human VL
C 25	15	93.8	23	4	ABN87313	Abn87313 Human VL
C 26	15	93.8	23	6	ABK51881	PCR prime
C 27	15	93.8	23	6	ABT76655	Novel met
C 28	15	93.8	23	6	AAD28826	Human ant
C 29	15	93.8	23	6	ABQ78094	Huvkp rel
C 30	15	93.8	23	6	ABQ78088	Humanised
C 31	15	93.8	23	6	ABQ82771	K+betaM3
C 32	15	93.8	23	6	ABK15777	Mutation
C 33	15	93.8	23	6	ABQ65581	Human imm
C 34	15	93.8	23	6	ABQ81513	Human HGP
C 35	15	93.8	23	6	ABT09832	K+beta M6
C 36	15	93.8	23	6	ABK93305	PCR prime
C 37	15	93.8	23	6	ABX0178	12BS scPv
C 38	15	93.8	23	6	ABK12539	Humanised
C 39	15	93.8	23	6	ABT71384	Thrombopo
C 40	15	93.8	23	6	AAD12437	Human HDG
C 41	15	93.8	23	6	AAD16089	Human K+b
C 42	15	93.8	23	6	AAD10859	PCR prime
C 43	15	93.8	23	6	AAL19677	Anti-HGP
C 44	15	93.8	23	6	AAK98432	Human V g
C 45	15	93.8	23	6	ADJ33361	Human VL

RESULT 1
ID ABN84079 standard; DNA; 16 BP.
XX
AC ABN84079;
XX DT 23-SEP-2002 (first entry)
XX DB FR1 collar sequence.
XX OS Unidentified.
XX PN WO200246435-A2.
XX PD 13-JUN-2002.
XX PP 05-DEC-2001; 2001WO-US047452.
XX PR 05-DEC-2000; 2000US-0251440P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Bowdish KS, Barbas-Fredrickson S, Lin Y, Renshaw M, Wild M;
PI McWhirter J,
DR WP; 2002-537569/57.

The present sequence is an antibody framework region 1 (FR1) collar oligonucleotide that is used in the engineering of plasmids of the invention, especially plasmid PR5-CAT (see Abn84079); for the in situ production, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences.

Claim 35; Page 18; 65pp; English.

CC The present sequence is an antibody framework region 1 (FR1) collar oligonucleotide that is used in the engineering of plasmids of the invention, especially plasmid PR5-CAT (see Abn84079); for the in situ production, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences.

CC portion of an antibody can be directly incorporated into a plasmid by reverse transcription of mRNA. The plasmid is engineered to contain 2 template annealing sequences, i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 399.193 Seconds
(without alignment(s))
1942.126 Million cell updates/sec

Title: US-10-006-591A-3

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Sequence: 1 99gtcatctggatgt 16

Scoring table: IDENTITY_NUC
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Searched: 4708333 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: 9b_om:*
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6: 9b_pat:*
7: 9b_ph:*
8: 9b_pl:*
9: 9b_pr:*
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11: 9b_sts:*
12: 9b_sy:*
13: 9b_un:*
14: 9b_vl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	15	93.8	16	6	AX642151	AX642151 Sequence
c 2	15	93.8	18	6	AR077364	AR077364 Sequence
c 3	15	93.8	18	6	AR117984	AR117984 Sequence
c 4	15	93.8	18	6	I95705	I95705 Sequence 33
c 5	15	93.8	18	6	AR265427	AR265427 Sequence
c 6	15	93.8	20	6	AR876236	AR876236 Sequence
c 7	15	93.8	20	6	AR476248	AR476248 Sequence
c 8	15	93.8	20	6	BD077342	BD077342 Method of
c 9	15	93.8	20	6	BD077354	BD077354 Method of
c 10	15	93.8	21	6	AR105680	AR105680 Sequence
c 11	15	93.8	21	6	AR09374	AR09374 Sequence
c 12	15	93.8	21	6	AR306562	AR306562 Sequence
c 13	15	93.8	21	6	AX740319	AX740319 Sequence
c 14	15	93.8	21	6	AX740320	AX740320 Sequence
c 15	15	93.8	21	6	BD105911	BD105911 Immuno-cox
c 16	15	93.8	23	6	A27361	A27361 Oligonucleo
c 17	15	93.8	23	6	A32955	A32955 Synthetic P
c 18	15	93.8	23	6	A33874	A33874 Synthetic P
c 19	15	93.8	23	6	A38167	A38167 Sequence 11

ALIGNMENTS

RESULT	1	AX642151	LOCUS	Sequence 3 from Patent WO246435.	DEFINITION	16 bp	DNA	linear	PAT	21-FEB-2003
			AX642151	Sequence 3	from Patent WO246435.					
			AX642151	Accession						
			AX642151	Version						
			AX642151.1	GI:28474639						
					KEYWORDS					
					Synthetic construct					
					synthetic construct					
					other sequences; artificial sequences.					
					REFERENCE					
					Bowdish, K.S., Barbas-Fredrickson, S., Lin, Y.C., Renshaw, M., Wild, M.					
					and McWhirter, J.					
					TITLE					
					Engineered Peptamides and their use for in situ production of genes					
					JOURNAL					
					ALEXION PHARMACEUTICALS, INC. (US)					
					FEATURES					
					Source					
					ORGANISM					
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					other sequences; artificial sequences.					
					REFERENCE					
					1					
					ORIGIN					
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						Best Local Similarity	100.0%	Pred. No.	3-5e-02;	
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							/note="m is unassigned DNA"			
							/note="xref="taxon:32630"			
							/note="collar sequence"			
							16			

RESULT	2	AR077364/C	LOCUS	Sequence 79 from patent US 5962255.	DEFINITION	18 bp	DNA	linear	PAT	31-AUG-2000
			AR077364	Sequence 79	from patent US 5962255.					
			AR077364	Accession						
			AR077364	Version						
			AR077364.1	GI:10004110						
					KWYORDS					